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FIG. 1A

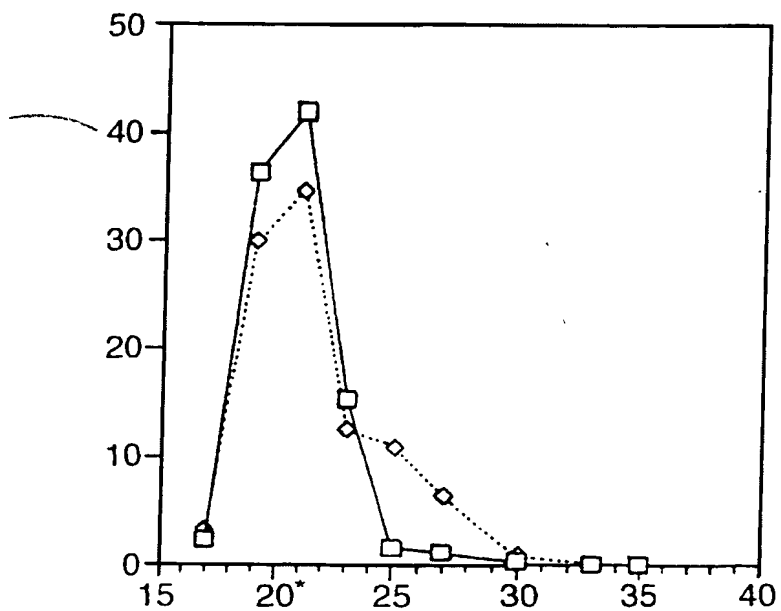
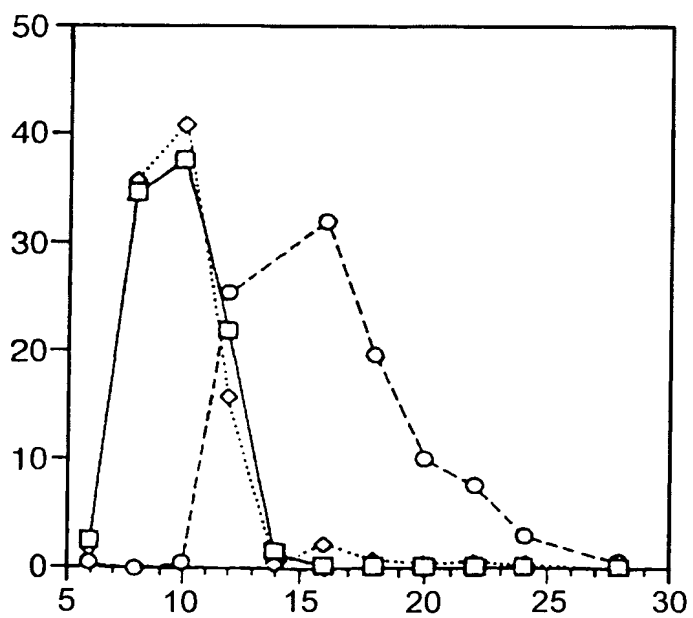
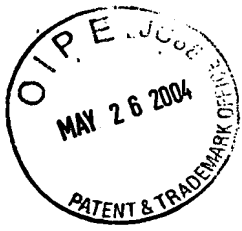


FIG. 1B





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sCLIG4 1 MISALDSIPEPQNFAPSPDFKWLCEELFKVIHEVQINCTAGTGRSRSEFKYIEIISNFVEMWRKTVGNNIYPALPFRDRRINIKOYVIRTRTICSVYKLPKNSATEQRLKDWKQVRVG
hLIGIVMRHILPOLERERMANGIKETMARLYIELNLPDRGKDALRILNRYTRPTG

sCLIG4 121 KGENLSILLVEE..IAKRRAPSSKAITIDNVNHYLDLSGDRFASGRGFRSIVKSKPFIHCVENNSFVELKVFEDIVLKNRVICQOEKHLNLCWHPPDAQDYL5VLSIKVVTSKYDEK
hLIGIV 51 THGADGFAMIAFYVLKPRCLOKG.SLTIQOVNDLDSIASNNSAKR...KOLIK.KSLIOLITQSSALECKWLIRMIIKOLKLGVSQQTIFSVFHDAAELHNVTDDIEKVCRLHDS

sCLIG4 239 VRLKDDLSIKVGFAPOLAKKVNLSYEMICRTL..HDDLVEKMDGERIQVHYMYNCEISIKFESRRGIDITYLYGASLSSGTSISOHLR..FTDSVKBQVLDGEMVTFDAKRVILPFG
hLIGIV 166 VGI...SDISITLFSASKPMALALADI...BHEKOMKHQSEYIEIKLDGERQOH..KQDQVYKVESRNGYNTDQFGASPTESLTPFIHNAEKADIQICILDGEMAYNPNTQTTFMQK

sCLIG4 356 LVKSAKEALSFNINNVDFFPIYAVFDLTYINGTSPLPLPHQKQYINLSLPLKNIVEIVRSRCYGVESIKKSDEVAISLSEGVVLRTYNSYNVASRNNMTIKVKPEYLEEFG
hLIGIV 280 TKFDIKRM.....VEDSDLOQCYCVFEDVAVNNKULGHETIRKYEILSSITPIPGRIEIVQKTOAHTXNEVIDA..NEADKREEGIMVQPLSIYKPKRGEGLKIKPEVSGIMD

sCLIG4 476 NDDLIVIG..RDSCKDSFMLGLFVLDEBEYKKHQDSSEIVDHSQEKHIQNSRRRVKILSFCSIANCISQZEFKEIDRKTRGHMKRTSEVAPPASTIDEFGSKLPAZWIDPSESIVLE
hLIGIV 394 EDDLIVGCGYWGKSGRGCMASHFCAVAE..KPPPEKPSVFH.....TISRVGSCCTMKELYDLGILAKLYWKPFHRKAPPSIL..CGTEREYVYIEPCNSVIVQ

sCLIG4 594 IKRSRLDNTETNMOKVATNCTFYGGYCKRIRYDKEMTDGYTLANDLYESRTVKS.....NPSYQAEBSQLGLIRKRRKRVILSDSTHONRKQL.FISNIFAGLLEYVLSDYVTE
hLIGIV 492 IKAIEIVPSD...NKTGCTFRFPRIERIRDDKEWHECMTDDLEQLRGKASGLASKHLYIGGDDEPOKRRKAAPKMKVIGIIEHLKAPNLTNVKNLSNIPEDVEECVA-SCGDSQ.

sCLIG4 702 TGIRITRAELEKTVHEHGCKLIYNVILKRHSIGDVRLISCKTTTECKAII..DRGYDILHENWVLDGIAYKRLILLIEBNTCFNVSQKRAVAEKRVDCIGDSFENDISETKLSLYKSQLS
hLIGIV 607KPPOLENRJAEFGG.....YIVQNPQPDITYCVLAGSENIRVKNILSNKHQVVKBAWLECFKTKSFVPQPERMIHMCPSKEHFAREYDCIGDSYFIDTDLNOLKEVFSGIRN

sCLIG4 821 LPPMGELEIDSEVRRF.....PFLFSNRJIAVPR...RKISTEDDIEMTKLFGCKITDQQSLCNLIIIPYTDPILRDCMNEVEKIKEQIKASDTIPKJARVVAPEWVDHS
hLIGIV 717 SNEQTPEEMASLIADLEYRYSWDCSPLSMRBHTVWLD SYAVINDLSTKNEGTRLAJKALELRTHGAK.....VVSCLAEGVSHVIGEDISRVADFKAFRRFTFRKFKILKE5WVTD5

sCLIG4 928 INENCQVFEEDFFVVNY*
hLIGIV 831 I.DKQELQENQYLI*

FIG. 2

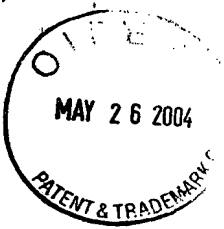


FIG. 3A

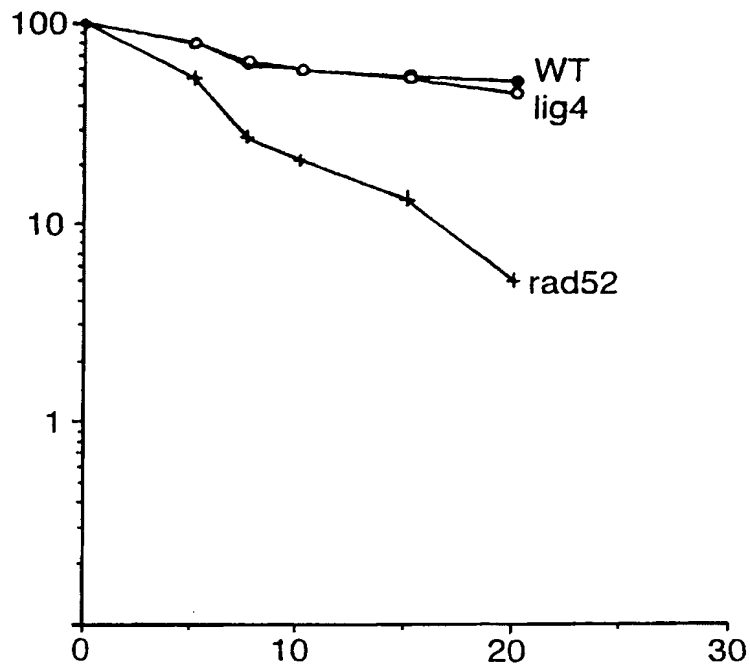


FIG. 3B

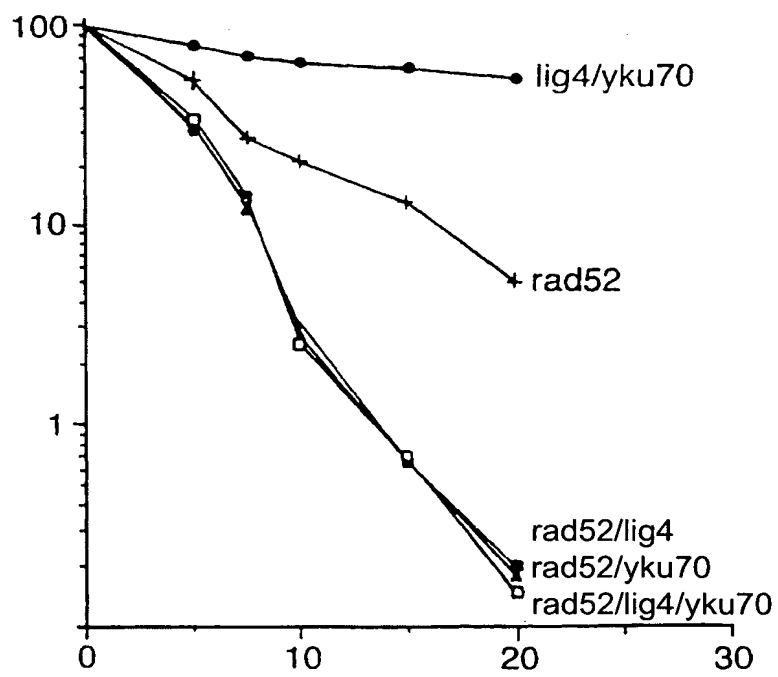




FIG. 4

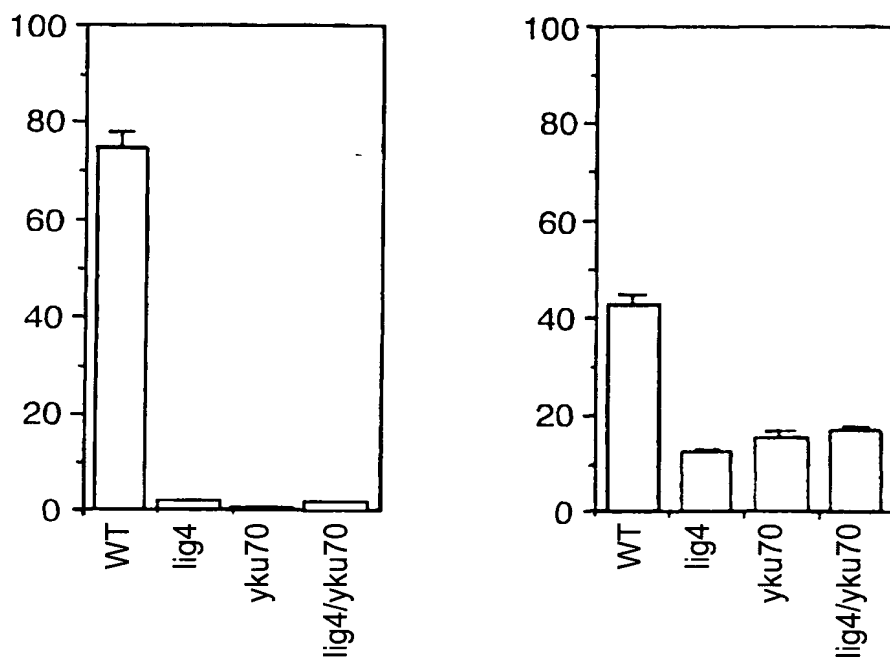
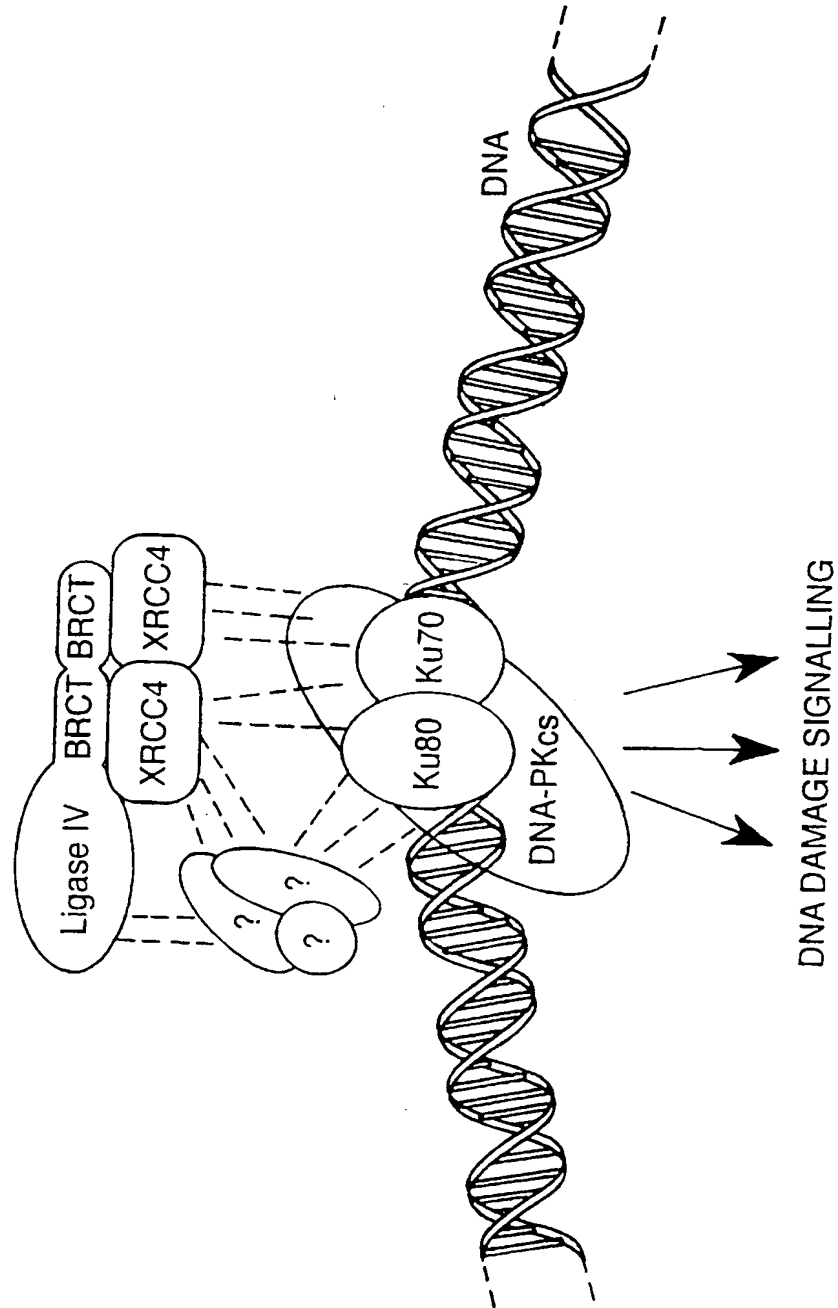


FIG. 5





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FIG. 6

GTGATTAAATAGGCTGAAATCAGTGTITAGTAACTACGTACGTTGTACATGTAACATTGT
1 -----+-----+-----+-----+-----+-----+-----+ 60
CACTAATTTATCCGACTTTAGTCACAAATCATTGATGCATGCAACATGTACATTGTAACA
V I K * A E I S V * * L R T L Y M * H C -
GATATAAATCGTAAGATTTCGCCGAGTATAGATCAATAATATCGGTTTCATCACTTACGTT
61 -----+-----+-----+-----+-----+-----+-----+ 120
CTATATTTAGCATTCTAAGCGGCTCATATCTAGTTATTATAGCCAAAGTAGTGAATGCAA
D I N R K I R R V * I N N I G F I T Y V -
GTTTGTGCAGTACTAGAGTTAAGATCGTTTTTCGATCCCTTATTTTCTTCTTTTTTCTCTTT
121 -----+-----+-----+-----+-----+-----+-----+ 180
CAAACACGTCATGATCTCAATTCTAGCAAAGCTAGGGAATAAAAGAAGAAAAAGGAAA
V C A V L E L R S F S I P Y F L L F S F -
TTTTTGTATTTTTTCTCTTTTTTACCTTTTGTGCACCATATTAAATCTTTAAACAAATCTAA
181 -----+-----+-----+-----+-----+-----+-----+ 240
AAAAACAATAAAAAGAGAAAAATGGAACAGTGGTATAATTTAGAAATTTGTTTAGATT
F L L F F S F Y L L S P Y * I F K Q I * -
CTATGAAAAATCCTTTAAACATATGTTAATATGTGGAAAAATAAATACTAAAAATAAAAT
241 -----+-----+-----+-----+-----+-----+-----+ 300
GATACTTTTTTAGGAAATTTGTATACAATTATACACCTTTTATTTATGATTTTATTTTAA
L * K N P L N I C * Y V E N K Y * N K N -
CTAGAAGTGAAGGAAATAGTAACGGATTATTTAGGTATGATATCAGCACTAGATTCTATA
301 -----+-----+-----+-----+-----+-----+-----+ 360
GATCTTGACTTCCTTTATCATTGCCTAATAAATCCATACTATAGTCGTGATCTAAGATAT
L E L K E I V T D Y L G M I S A L D S I -
CCCGAGCCCCAAAACCTTTGCGCCTAGTCCAGATTTCAAATGGCTTTGTGAAGAGCTATTT
361 -----+-----+-----+-----+-----+-----+-----+ 420
GGGCTCGGGGTTTTGAAACGCGGATCAGGTCTAAAGTTTACCGAAACACTTCTCGATAAA
P E P Q N F A P S P D F K W L C E E L F -
GTGAAGATACATGAAGTTCAAATTAATGGAACGGCCGGCACTGGCAAATCAAGGTCTTTTC
421 -----+-----+-----+-----+-----+-----+-----+ 480
CACTTCTATGTACTTCAAGTTTAATTACCTTGCCGGCCGTGACCGTTTAGTTCCAGAAAG
V K I H E V Q I N G T A G T G K S R S F -
AAGTACTATGAAATAATATCGAATTTTCGTCGAAATGTGGAGAAAAACCGTGGGAAATAAT
481 -----+-----+-----+-----+-----+-----+-----+ 540
TTCATGATACCTTTATTATAGCTTAAAGCAGCTTTACACCTCTTTTTTGGCACCCCTTTATTA
K Y Y E I I S N F V E M W R K T V G N N -
ATATATCCTGCACTGGTTCTTGCTCTTCCTACCGGATAGACGAATCTATAATATTAAG
541 -----+-----+-----+-----+-----+-----+-----+ 600
TATATAGGACGTGACCAAGAACGAGAAGGGATGGCGCTATCTGCTTAGATATTATAATTC
I Y P A L V L A L P Y R D R R I Y N I K -



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FIG. 6 (CONT.)

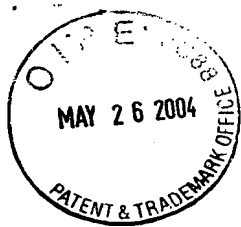
601 GATTATGTATTAAATAAGAACTATATGCTCTTACTTGAAGTTGCCAAAAAATTCTGCAACA 660
CTAATACATAATTATCTTTGATATACGAGAATGAACTTCAACGGTTTTTTAAGACGTTGT
D Y V L I R T I C S Y L K L P K N S A T -
661 GAGCAGCGGTTAAAAGATTGGAAACAGCGTGTGGTAAAGGTGGGAATCTTTCTCTCTT 720
CTCGTGGCAATTTTCTAACCTTTGTGCGCACAGCCATTTCCACCCTTAGAAAGAAGAGAA
E Q R L K D W K Q R V G K G G N L S S L -
721 CTGTGGAAGAAATTGCTAAAAGAAGGGCTGAACCTAGCTCAAAAGCGATTACAATTGAT 780
GAACACCTTCTTTAACGATTTTCTTCCGACTTGGATCGAGTTTTCGCTAATGTTAACTA
L V E E I A K R R A E P S S K A I T I D -
781 AACGTCAATCACTATCTGGATAGTTTGTAGTGGAGACAGGTTTCGCTTCCGGACGAGGATTT 840
TTGCAGTTAGTGATAGACCTATCAAACCTCACCTCTGTCCAAGCGAAGGCCTGCTCCTAAA
N V N H Y L D S L S G D R F A S G R G F -
841 AAGAGTCTTGTCAAGTCCAAACCTTTCTGCACTGTGTGGAGAATATGAGTTTCGTGCGAA 900
TTCTCAGAACAGTTCAGGTTTGGAAAGGACGTGACACACCTCTTATACTCAAAGCAGCTT
K S L V K S K P F L H C V E N M S F V E -
901 TTAAAATACTTCTTTGATATCGTGCTTAAAAATAGAGTAATAGGAGGTCAAGAGCACAAA 960
AATTTTATGAAGAACTATAGCACGAATTTTATCTCATTATCCTCCAGTTCTCGTGTTT
L K Y F F D I V L K N R V I G G Q E H K -
961 TTGCTAAACTGCTGGCATCCTGATGCTCAGGATTATCTTAGCGTGATATCTGATTTAAAG 1020
AACGATTTGACGACCGTAGGACTACGAGTCCTAATAGAATCGCACTATAGACTAAATTTT
L L N C W H P D A Q D Y L S V I S D L K -
1021 GTGGTAACTTCAAACTTTATGATCCAAAAGTTCGTCTAAAGGATGATGATTTGAGTATA 1080
CACCATTGAAGTTTTGAAATACTAGGTTTTTCAAGCAGATTTCTACTACTAAACTCATAT
V V T S K L Y D P K V R L K D D D L S I -
1081 AAAGTTGGCTTTGCAATTCGCCCCCAATTAGCCAAAAAGTGAATCTTTCTTATGAGAAA 1140
TTTCAACCGAAACGTAAGCGGGGGTTAATCGGTTTTTTCACCTTAGAAGAATACTCTTT
K V G F A F A P Q L A K K V N L S Y E K -
1141 ATATGCCGTACACTACATGATGATTTTTTGGTAGAAGAAAAATGGATGGAGAACGAATT 1200
TATACGGCATGTGATGTACTACTAAAAAACCATCTTCTTTTTTACCTACCTCTTGCTTAA
I C R T L H D D F L V E E K M D G E R I -
1201 CAAGTTTATTATATGAATTATGGTGAATCCATAAAATTTTTTAGTAGACGGGGCATCGAC 1260
GTTCAAGTAATATACTTAATACCACTTAGGTATTTTAAAAAATCATCTGCCCCGTAGCTG
Q V H Y M N Y G E S I K F F S R R G I D -



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FIG. 6 (CONT.)

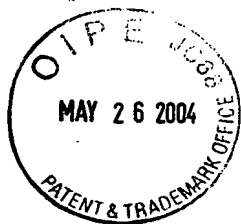
1261 TATACCTATTTGTACGGAGCGAGCTTATCATCAGGAACCTATATCTCAACATTTGAGGTTT 1320
-----+-----+-----+-----+-----+
ATATGGATAAACATGCCTCGCTCGAATAGTAGTCCTTGATATAGAGTTGTAAACTCCAAA
Y T Y L Y G A S L S S G T I S Q H L R F -
1321 ACAGATAGTGTAAAGAATGTGTTTTAGATGGAGAAATGGTGACGTTTGATGCAAAAAGA 1380
-----+-----+-----+-----+-----+
TGTCTATCACAATTTCTTACACAAAATCTACCTCTTTACCACTGCAAACTACGTTTTTCT
T D S V K E C V L D G E M V T F D A K R -
1381 CGGGTGATTCTTCCATTCCGGTCTTGTTAAAGGAAGTGCAAAGGAAGCGCTATCTTTTAAT 1440
-----+-----+-----+-----+-----+
GCCCCACTAAGAAGGTAAGCCAGAACAATTTCCCTTCACGTTTCCTTCGCGATAGAAAATTA
R V I L P F G L V K G S A K E A L S F N -
1441 AGTATAAATAATGTTGACTTTTACCCCTTATATATGGTGTMTGATCTGTTATACCTGAAT 1500
-----+-----+-----+-----+-----+
TCATATTTATTACAACTGAAAGTGGGGAATATATACCACAACTAGACAATATGGACTTA
S I N N V D F H P L Y M V F D L L Y L N -
1501 GGGACTTCGTTGACACCATTAACCCCTTCATCAAAGGAAGCAATATCTGAACAGCATTTTA 1560
-----+-----+-----+-----+-----+
CCCTGAAGCAACTGTGGTAATGGGAAGTAGTTTCCTTCGTTATAGACTTGTGTAATAAT
G T S L T P L P L H Q R K Q Y L N S I L -
1561 AGTCCCTTGAAAAATATTTGTAGAAATAGTAGCATCTTCTAGATGTTATGGTGTGGAGTCA 1620
-----+-----+-----+-----+-----+
TCAGGGAACTTTTATAACATCTTTATCATGCTAGAAGATCTACAATACCACACCTCAGT
S P L K N I V E I V R S S R C Y G V E S -
1621 ATCAAAAAGTCTTTAGAAGTTGCAATCTCACTGGGTTGAGAAGGAGTTGTTTTGAAATAT 1680
-----+-----+-----+-----+-----+
TAGTTTTTCAGAAATCTTCAACGTTAGAGTGACCCAAGTCTTCCTCAACAAAACTTTTATA
I K K S L E V A I S L G S E G V V L K Y -
1681 TATAATTCAAGTTATAATGTGCCAGTCGAAACAACAACCTGGATCAAGGTAAAACCTGAA 1740
-----+-----+-----+-----+-----+
ATATTAAAGTTCAATATTACAGCGGTCAGCTTTGTTGTTGACCTAGTTCCATTTTGGACTT
Y N S S Y N V A S R N N N W I K V K P E -
1741 TATTTGGAGGAATTTGGAGAGAATTTAGACTTAATAGTAATAGGCAGAGATTCTGGGAAA 1800
-----+-----+-----+-----+-----+
ATAAACCTCCTTAAACCTCTCTTAAATCTGAATTATCATTATCCGTCTCTAAGACCCCTT
Y L E E F G E N L D L I V I G R D S G K -
1801 AAAGATTCTTTTATGCTAGGGTTACTTGTGCTAGATGAAGAAGAGTATAAAAAGCACCAA 1860
-----+-----+-----+-----+-----+
TTTCTAAGAAAATACGATCCCAATGAACACGATCTACTTCTTCTCATATTTTTCGTGGTT
K D S F M L G L L V L D E E E Y K K H Q -
1861 GGAGACTCCTCTGAAATTGTAGACCACTCAAGCCAAGAAAAACACATACAAAATTCAGA 1920
-----+-----+-----+-----+-----+
CCTCTGAGGAGACTTTAACATCTGGTGAGTTCCGTTCTTTTTGTGTATGTTTTAAGTTCT
G D S S E I V D H S S Q E K H I Q N S R -
AGAAGGGTGAAAAAATACTTTTCATTCTGTTCTATCGCAACCGGTATATCTCAAGAAGAA



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FIG. 6 (CONT.)

1921 -----+-----+-----+-----+-----+ 1980
TCTTCCCACTTTTTTATGAAAGTAAGACAAGATAGCGTTTGCCATATAGAGTTCTTCTT
R R V K K I L S F C S I A N G I S Q E E -
TTCAAAGAAATCGACCGCAAAACGAGAGGACATTGGAAAAGAACCTCCGAAGTTGCTCCC
1981 -----+-----+-----+-----+-----+ 2040
AAGTTTCTTTAGCTGGCGTTTGTCTCTCTGTAAACCTTTTCTTGGAGGCTTCAACGAGGG
F K E I D R K T R G H W K R T S E V A P -
CCTGCTTCAATTTTAGAATTTGGCTCAAAAATACCTGCCGAATGGATTGACCCAGTGAA
2041 -----+-----+-----+-----+-----+ 2100
GGACGAAGTTAAAATCTTAAACCGAGTTTTTATGGACGGCTTACCTAACTGGGGTCACTT
P A S I L E F G S K I P A E W I D P S E -
TCAATTTGTTCTAGAAATAAAATCACGGTCTTTGGATAACACAGAAACGAATATGCAGAAG
2101 -----+-----+-----+-----+-----+ 2160
AGTTAACAAGATCTTTATTTTAGTGCCAGAAACCTATTGTGTCTTTGCTTATACGTCTTC
S I V L E I K S R S L D N T E T N M Q K -
TACGCTACCAATTGTACTTTGTACGGTGGCTATTGTAAAAGAATACGGTACGATAAAGAA
2161 -----+-----+-----+-----+-----+ 2220
ATGCGATGGTTAACATGAAACATGCCACCGATAACATTTTCTTATGCCATGCTATTTCTT
Y A T N C T L Y G G Y C K R I R Y D K E -
TGGACAGATTGTTACACACTTAACGACTTATACGAAAGTAGGACGGTTAAATCTAACCCC
2221 -----+-----+-----+-----+-----+ 2280
ACCTGTCTAACAATGTGTGAATTGCTGAATATGCTTTTCATCCTGCCAATTTAGATTGGGG
W T D C Y T L N D L Y E S R T V K S N P -
AGCTATCAAGCGGAAAGGTCACAGCTTGGATTGATACGGAAAAAGAGAAAGAGAGTACTT
2281 -----+-----+-----+-----+-----+ 2340
TCGATAGTTGCGCTTTCCAGTGTGGAACCTAACTATGCCTTTTTCTCTTTCTCTCATGAA
S Y Q A E R S Q L G L I R K K R K R V L -
ATTTTCAGACAGCTTTTACCAAAACAGGAAACAACCTGCCAATTTTCAAACATCTTTGCCGGA
2341 -----+-----+-----+-----+-----+ 2400
TAAAGTCTGTGGAAGTGGTTTTGTCTTTTGTGACGGTTAAAGTTTGTAGAAACGGCCT
I S D S F H Q N R K Q L P I S N I F A G -
TTACTTTTTTATGTTCTCTCTGACTATGTACGGAGGACACTGGAATACGGATTACACGG
2401 -----+-----+-----+-----+-----+ 2460
AATGAAAAAATACAAGAGAGACTGATACAGTGCCTCCTGTGACCTTATGCCTAATGTGCC
L L F Y V L S D Y V T E D T G I R I T R -
GCAGAACTTGAAAAAACTATTGTGGAACATGGTGGTAAACTGATATATAATGTAATTTTA
2461 -----+-----+-----+-----+-----+ 2520
CGTCTTGAACTTTTTTGATAACACCTTGTACCACCATTTGACTATATATTACATTAAAT
A E L E K T I V E H G G K L I Y N V I L -
AAACGTCATTCAATTGGGGACGTTGCGTTAATCAGCTGTAAAACTACCACGGAATGCAAG
2521 -----+-----+-----+-----+-----+ 2580
TTTGACAGTAAGTTAACCCTGCAAGCCAATTAGTCGACATTTTGATGGTGCCTTACGTTT
K R H S I G D V R L I S C K T T T E C K -
GCTTTAATAGATCGAGGATATGATATATTGACCCAAATTTGGTACTCGATTGTATAGCA
2581 -----+-----+-----+-----+-----+ 2640



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FIG. 6 (CONT.)

CGAAATTATCTAGCTCCTATACTATATAACGTGGGTTTAACCCATGAGCTAACATATCGT
A L I D R G Y D I L H P N W V L D C I A -
TATAAGAGGCTCATCCTGATCGAGCCCAATTATTGCTTTAACGTCTCTCAAAAAATGAGA
2641 -----+-----+-----+-----+-----+ 2700
ATATTCTCCGAGTAGGACTAGCTCGGGTTAATAACGAAATTGCAGAGAGTTTTTTACTCT
Y K R L I L I E P N Y C F N V S Q K M R -
GCCGTCGCTGAAAAAAGGTTAGATTGTTTGGGTGATAGTTTGTGAAAATGACATTTCGGAA
2701 -----+-----+-----+-----+-----+ 2760
CGGCAGCGACTTTTTTCCCATCTAACAAACCCACTATCAAAACTTTTACTGTAAAGCCTT
A V A E K R V D C L G D S F E N D I S E -
ACCAAACGTGCATCATTTGTATAAATCACAACCTAAGTCTACCACCGATGGGGGAACCTCGAG
2761 -----+-----+-----+-----+-----+ 2820
TGGTTTGACAGTAGTAACATATTTAGTGTGATTCAGATGGTGGCTACCCCTTGAGCTC
T K L S S L Y K S Q L S L P P M G E L E -
ATAGATTCTGAGGTTTCGGCGGTTTCCATTATTTTTATTCTCCAACAGGATTGCATACGTA
2821 -----+-----+-----+-----+-----+ 2880
TATCTAAGACTCCAAGCCGCCAAAGGTAATAAAATAAGAGGTTGTCTAACGTATGCAT
I D S E V R R F P L F L F S N R I A Y V -
CCACGTCGCAAAATTAGCACAGAAGATGACATTATAGAAATGAAAATTAAGTTGTTTGGT
2881 -----+-----+-----+-----+-----+ 2940
GGTGACGCGTTTTTAATCGTGTCTTCTACTGTAATATCTTTACTTTTAAATCAACAAACCA
P R R K I S T E D D I I E M K I K L F G -
GGAAAAATAACAGATCAACAGTCACCTTTGTAACCTAATAATTATACCATATACTGATCCT
2941 -----+-----+-----+-----+-----+ 3000
CCTTTTTATTGTCTAGTTGTCTAGTGAAACATTGAATTATTAATATGGTATATGACTAGGA
G K I T D Q Q S L C N L I I I P Y T D P -
ATTTTGAGGAAAGACTGCATGAATGAGGTACACGAAAAAATAAAAGAACAAATAAGGCT
3001 -----+-----+-----+-----+-----+ 3060
TAAACTCCTTTCTGACGTACTTACTCCATGTGCTTTTTTATTTCCTGTGTTTATTTCCGA
I L R K D C M N E V H E K I K E Q I K A -
TCTGATACTATACCGAAAAATAGCCAGGGTCGTTGCCCTGAATGGGTGGATCATTCTATT
3061 -----+-----+-----+-----+-----+ 3120
AGACTATGATATGGCTTTTTATCGGTCCAGCAACGGGGACTTACCCACCTAGTAAGATAA
S D T I P K I A R V V A P E W V D H S I -
AATGAAAACGTGTCAAGTGCCTGAAGAAGACTTCCCCGTAGTCAACTACTGATGGTGGGTT
3121 -----+-----+-----+-----+-----+ 3180
TTACTTTTGACAGTTACGGACTTCTTCTGAAGGGGCATCAGTTGATGACTACCACGCAA
N E N C Q V P E E D F P V V N Y * W C V -
TTGCGGAGGCTTAATTTTTTGAAGTTTATTTAATACTATCCTACATATGTACATTAAATA
3181 -----+-----+-----+-----+-----+ 3240
AACGCCCTCCGAATTAAAAAATTCAAAATAAATTATGATAGGATGTATACATGTAATTTAT
L R R L N F L K F I * Y Y P T Y V H * I -
CTTCGTAAAGTTTATCAATAAGAGTGGAAGATGGCAATTATATTCAAAAGATTGGCCA
3241 -----+-----+-----+-----+-----+ 3300
GAAGGCATTGCAAAATAGTTATTCTCACCTTCTAAGGTTAATATAAGTTTTCTAACCGGT



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FIG. 6 (CONT.)

L P * R L S I R V E D A Q L Y S K D W P -

3301 GTCAATTAACTTAAGGAAAAAAT
-----+-----+----- 3323
CAGTTAATTGAATTCCTTTTITA

V N * L K E K